



SEQUENCE LISTING

<110> He Sonnewald
Marcus Ebneith

<120> 2-Deoxyglucose-6-phosphate (2-DOG-6-P) phosphatase DNA sequences as
selection marker in plants

<130> VOS-12 CON

<140> 09/558,284

<141> 2000-04-25

<150> PCT/EP98/02069

<151> 1998-04-09

<160> 4

<170> PatentIn Release #1.0, Version #1.30 (EPO)

<210> 1

<211> 758

<212> DNA

<213> *Saccharomyces cerevisiae*

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GGT	ACC	ATA	GTG	AGT	ACA	ACA	GTG	GCC	GCA	GAG	AAA	GCA	TGG	ACC	AAG	98
Gly	Thr	Ile	Val	Ser	Thr	Thr	Val	Ala	Ala	Glu	Lys	Ala	Trp	Thr	Lys	
15				20				25					30			
TTG	TGT	TAC	GAA	TAC	GGT	GTT	GAT	CCT	TCC	GAG	TTA	TTT	AAG	CAT	TCT	146
Leu	Cys	Tyr	Glu	Tyr	Gly	Val	Asp	Pro	Ser	Glu	Leu	Phe	Lys	His	Ser	
				35				40					45			
CAT	GGT	GCA	AGA	ACA	CAA	GAG	GTT	TTG	AGA	AGG	TTT	TTC	CCT	AAA	TTG	194
His	Gly	Ala	Arg	Thr	Gln	Glu	Val	Leu	Arg	Arg	Phe	Phe	Pro	Lys	Leu	
			50					55					60			
GAT	GAT	ACA	GAC	AAT	AAA	GGT	GTT	CTT	GCT	CTA	GAA	AAA	GAT	ATT	GCC	242
Asp	Asp	Thr	Asp	Asn	Lys	Gly	Val	Leu	Ala	Leu	Glu	Lys	Asp	Ile	Ala	
			65				70					75				
CAT	AGT	TAC	TTG	GAT	ACA	GTA	AGC	CTT	ATT	CCT	GGT	GCA	GAG	AAC	TTA	290
His	Ser	Tyr	Leu	Asp	Thr	Val	Ser	Leu	Ile	Pro	Gly	Ala	Glu	Asn	Leu	
	80					85					90					

CTG	TTA	TCG	TTA	GAT	GTA	GAT	ACT	GAG	ACT	CAA	AAA	AAG	TTA	CCT	GAA	338
Leu	Leu	Ser	Leu	Asp	Val	Asp	Thr	Glu	Thr	Gln	Lys	Lys	Leu	Pro	Glu	
95					100					105					110	
AGG	AAA	TGG	GCT	ATC	GTT	ACC	TCT	GGT	TCT	CCA	TAT	TTG	GCA	TTT	TCA	386
Arg	Lys	Trp	Ala	Ile	Val	Thr	Ser	Gly	Ser	Pro	Tyr	Leu	Ala	Phe	Ser	
			115					120						125		
TGG	TTC	GAG	ACA	ATA	TTG	AAA	AAT	GTT	GGA	AAG	CCC	AAA	GTT	TTC	ATT	434
Trp	Phe	Glu	Thr	Ile	Leu	Lys	Asn	Val	Gly	Lys	Pro	Lys	Val	Phe	Ile	
			130					135						140		
ACT	GGG	TTT	GAC	GTG	AAG	AAC	GGT	AAG	CCT	GAT	CCC	GAG	GGT	TAT	TCA	482
Thr	Gly	Phe	Asp	Val	Lys	Asn	Gly	Lys	Pro	Asp	Pro	Glu	Gly	Tyr	Ser	
		145					150					155				
AGA	GCT	CGT	GAT	TTA	TTG	CGT	CAA	GAT	TTG	CAA	TTA	ACT	GGT	AAA	CAG	530
Arg	Ala	Arg	Asp	Leu	Leu	Arg	Gln	Asp	Leu	Gln	Leu	Thr	Gly	Lys	Gln	
	160					165						170				
GAT	CTG	AAG	TAT	GTT	GTC	TTC	GAA	GAT	GCA	CCC	GTG	GGC	ATA	AAG	GCC	578
Asp	Leu	Lys	Tyr	Val	Val	Phe	Glu	Asp	Ala	Pro	Val	Gly	Ile	Lys	Ala	
175					180					185					190	
GGC	AAA	GCA	ATG	GGC	GCC	ATT	ACT	GTG	GGT	ATA	ACA	TCC	TCG	TAT	GAC	626
Gly	Lys	Ala	Met	Gly	Ala	Ile	Thr	Val	Gly	Ile	Thr	Ser	Ser	Tyr	Asp	
			195						200					205		
AAG	AGC	GTT	TTA	TTT	GAC	GCA	GGA	GCA	GAT	TAT	GTA	GTC	TGT	GAT	TTG	674
Lys	Ser	Val	Leu	Phe	Asp	Ala	Gly	Ala	Asp	Tyr	Val	Val	Cys	Asp	Leu	
		210						215					220			
ACA	CAG	GTT	TCC	GTG	GTT	AAG	AAC	AAT	GAA	AAC	GGT	ATT	GTC	ATC	CAG	722
Thr	Gln	Val	Ser	Val	Val	Lys	Asn	Asn	Glu	Asn	Gly	Ile	Val	Ile	Gln	
		225					230					235				
GTA	AAC	AAC	CCT	TTG	ACA	AGG	GCC	TGAGTAGTCG	AC							758
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<212> PRT

<213> *Saccharomyces cerevisiae*

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Ile	Val	Ser	Thr	Thr	Val	Ala	Ala	Glu	Lys	Ala	Trp	Thr	Lys	Leu	Cys
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Tyr	Glu	Tyr	Gly	Val	Asp	Pro	Ser	Glu	Leu	Phe	Lys	His	Ser	His	Gly
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Ala Arg Thr Gln Glu Val Leu Arg Arg Phe Phe Pro Lys Leu Asp Asp
50 55 60

Thr Asp Asn Lys Gly Val Leu Ala Leu Glu Lys Asp Ile Ala His Ser
65 70 75 80

Tyr Leu Asp Thr Val Ser Leu Ile Pro Gly Ala Glu Asn Leu Leu Leu
85 90 95

Ser Leu Asp Val Asp Thr Glu Thr Gln Lys Lys Leu Pro Glu Arg Lys
100 105 110

Trp Ala Ile Val Thr Ser Gly Ser Pro Tyr Leu Ala Phe Ser Trp Phe
115 120 125

Glu Thr Ile Leu Lys Asn Val Gly Lys Pro Lys Val Phe Ile Thr Gly
130 135 140

Phe Asp Val Lys Asn Gly Lys Pro Asp Pro Glu Gly Tyr Ser Arg Ala
145 150 155 160

Arg Asp Leu Leu Arg Gln Asp Leu Gln Leu Thr Gly Lys Gln Asp Leu
165 170 175

Lys Tyr Val Val Phe Glu Asp Ala Pro Val Gly Ile Lys Ala Gly Lys
180 185 190

Ala Met Gly Ala Ile Thr Val Gly Ile Thr Ser Ser Tyr Asp Lys Ser
195 200 205

Val Leu Phe Asp Ala Gly Ala Asp Tyr Val Val Cys Asp Leu Thr Gln
210 215 220

Val Ser Val Val Lys Asn Asn Glu Asn Gly Ile Val Ile Gln Val Asn
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Asn Pro Leu Thr Arg Ala
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA sequence

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA sequence

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